



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

PATENT

1638
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AP
10/6/02

In the Application of:

SAVERIO CARL FALCO ET AL.

CASE NO.: BB1205 US NA

APPLICATION NO.: 09/464,528

GROUP ART UNIT: 1638

FILED: DECEMBER 15, 1999

EXAMINER: CYNTHIA E. COLLINS

FOR: S-ADENOSYL-L-METHIONINE
SYNTHETASE PROMOTER AND ITS USE
IN EXPRESSION OF TRANSGENIC
GENES IN PLANTS

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OCT 31 2002

TECH CENTER 1600/2900

Response

Commissioner of Patents and Trademarks
Washington, DC 20231

Sir:

This is in response to Office Action dated May 22, 2002 regarding the above-identified Office Action. Applicants respectfully request reconsideration and submit the following in support thereof.

In the Specification:

Please amend the specification, paragraph at page 7, lines 1-28, as follows:

01
Moreover, the skilled artisan recognizes that substantially similar nucleic acid sequences encompassed by this invention are also defined by their ability to hybridize, under moderately stringent conditions (for example, 0.5 X SSC, 0.1% SDS, 60° C) with the sequences exemplified herein, or to any portion of the nucleotide sequences reported herein and which are functionally equivalent to the promoter of the invention. Preferred substantially similar nucleic acid sequences encompassed by this invention are those sequences that are 80% identical to the nucleic acid fragments reported herein or which are 80% identical to any portion of the nucleotide sequences reported herein. More preferred are nucleic acid fragments which are 90% identical to the nucleic acid sequences reported herein, or which are 90% identical to any portion of the nucleotide sequences reported herein. Most preferred are nucleic acid fragments which are 95% identical to the nucleic acid sequences reported herein, or which are 95% identical to any portion of the nucleotide sequences reported herein. Sequence alignments and percent similarity calculations may be determined using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences